

13th Midwest Conference on Protein Folding, Assembly and Molecular Motions

Notre Dame Conference Center – McKenna Hall – University of Notre Dame

May 5, 2018

8:00 – 8:55 *Coffee, juice, and pastries*

8:55 – 9:00 *Opening Remarks* – Patricia L. Clark

Opening Plenary Speaker

9:00 – 9:30 *Probing the effect of the ribosome on the protein folding pathway using single-molecule chemo-mechanical folding*

Emily Guinn^{1,2} & Susan Marqusee¹

¹California Institute for Quantitative Biosciences, UC-Berkeley

²Department of Chemistry and Biochemistry, DePauw University

Proteins in the Cell

Chair: TBA

9:30 – 9:50 *Stress-induced molecular chaperone production depends on adaptive intracellular pH change*

Catherine G. Triandafillou¹, Aaron R. Dinner², D. Allan Drummond³

¹Biophysical Sciences Graduate Program, ²James Franck Institute, ³Department of Biochemistry and Molecular Biology, The University of Chicago

9:50 – 10:10 *Conformational dynamics of *Pseudomonas aeruginosa* penicillin binding protein*
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Neha Rana & Shahriar Mobashery

Department of Chemistry & Biochemistry, University of Notre Dame, Notre Dame, IN 46556

10:10 – 10:30 *Measuring and modulating the extent of polypeptide disorder*

Micayla A. Bowman¹, Josh A. Riback², Adam M. Zmyslowski⁴, Tobin R. Sosnick^{3,4} & Patricia L. Clark¹

¹Department of Chemistry & Biochemistry University of Notre Dame, Notre Dame, IN; ²Institute for Biophysical Dynamics, ³Department of Chemistry, ⁴Department of Biochemistry and Molecular Biology, The University of Chicago, Chicago, IL 60637, USA

10:30 – 10:50 *Coffee Break*

Protein Conformational Changes & Binding

Chair: TBA

10:50 – 11:10 *Unbiased Molecular Dynamics of 11 minute Timescale Drug Unbinding Reveals Transition State Stabilizing Interactions*

Samuel Lotz, Alex Dickson

Department of Biochemistry and Molecular Biology, Michigan State University, East Lansing, MI

11:10 – 11:30 *Structural insight into Neisseria meningitidis lactoferrin binding protein B's interaction with human lactoferrin*

Ravi Yadav^{1,2}, Srinivas Govindan³, Tommi White⁴, Srinivas Chakravarthy⁵, Jia Ma⁶, Nicholas Noinaj^{2,7}

¹Purdue University Interdisciplinary Life science, ²Department of Biological Sciences,

³Department of Biomedical Engineering, Purdue University, West Lafayette, IN, ⁴Department of Biochemistry, University of Missouri, Columbia, MO, ⁵BIO-CAT, Illinois Institute of Technology, Sector 18ID, Advanced Photon Source, Argonne National Laboratory, Lemont, IL,

⁶Biophysical Analysis Laboratory, Bindley Bioscience Center, Purdue University, West Lafayette, IN, ⁷Purdue Institute for Inflammation, Immunology and Infectious Disease, Purdue University, West Lafayette, IN

11:30 – 11:50 *A new protein conformational switch using human Cellular Retinol Binding Protein II as a template*

Alireza Ghanbarpour, Zahra Assar, Elizabeth Santos, Meisam Nosrati, Babak Borhan, James H. Geiger

Department of Chemistry, Michigan State University, East Lansing, MI

11:50 – 1:15 *Lunch*

1:15 – 2:40 *Poster Session*

Proteins and Membranes

Chair: TBA

2:40 – 3:00 *Towards high resolution structure prediction of beta-barrel membrane proteins*

Wei Tian, Meishan Lin, Hammad Naveed, Jie Liang

Department of Bioengineering, University of Illinois at Chicago, Chicago, IL

3:00 – 3:20 *Role of Packing Defects in the Stability and Function of a Helical-bundle Membrane-bound Enzyme*

Ruiqiong Guo[†], Seung-Gu Kang[‡], Zixuan Cang[§], Erin Deans[⊥], Guowei Wei[§] and Heedeok Hong^{*,†,||}

[†]Department of Chemistry, ^{||}Department of Biochemistry & Molecular Biology and [§]Department of Mathematics, Michigan State University, East Lansing, MI

[‡]Computational Biology Center, IBM Thomas J. Watson Research Center, Yorktown Heights, NY

[⊥]Department of Chemistry, Brandeis University, Waltham, MA

3:20 – 3:40 *Experiment and simulations find that partially disordered KcsA monomers fold and bind within the bilayer to form tetramers not withstanding off-pathway misfolded species*
Kevin C. Song¹, Eduardo Perozo^{1,2,3}, Benoît Roux^{1,2,3,4}, Tobin R. Sosnick^{1,2,3}
¹Graduate Program in the Biophysical Sciences, ²Institute for Biophysical Dynamics, ³Department of Biochemistry and Molecular Biology, ⁴Department of Chemistry, The University of Chicago, Chicago, IL

3:40 – 4:00 *Coffee Break*

Protein Aggregation

Chair: TBA

4:00 – 4:20 *A Multi-Scale Study of Amyloid Wild-Types and Mutants: Monomers, Oligomers, Fibrils*
Arthur O. Vale¹, Jacob Usadi¹, Sachin R. Natesh¹, Sarida Pratuangtham², Karl F. Freed³, Esmael J. Haddadian⁴
¹Physical Sciences Collegiate Division, ^{2,3}Department of Chemistry and James Frank Institute, ⁴Biological Sciences Collegiate Division, University of Chicago, Chicago, IL

4:20 – 4:40 *Fast relaxation imaging of protein structure, stability, and folding in biomaterial environments with variable crowding*
Jay M. Pittman, Atul K. Srivastava, Christopher T. Boughter, Bharat Somireddy Venkata, Joseph R. Sachleben and Stephen C. Meredith
Department of Pathology, University of Chicago, Chicago, IL

Closing Plenary Speaker

4:40 – 5:10 *Role of topological defects in membrane protein homeostasis*
Francis Roushar,¹ Timothy Gruenhagen,¹ Wesley D. Penn,¹ Beata Jastrzebska,² and Jonathan P. Schleich¹
¹Department of Chemistry, Indiana University, Bloomington, Indiana USA 47405
²Department of Pharmacology, Case Western Reserve University, Cleveland, Ohio 44106

5:10 – 5:15 *Closing Remarks – Connie Jeffrey*

5:15 – 6:30 *Closing Reception*